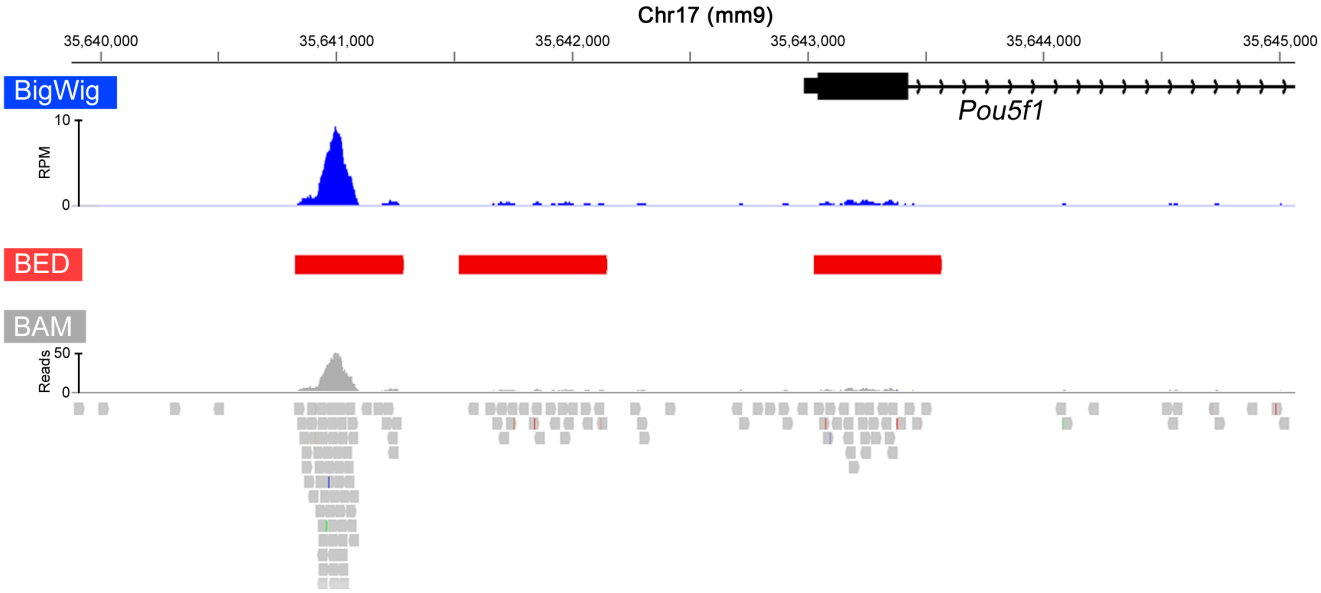
Chr17 (mm9)
35,640,000
35,641,000
35,642,000
35,643,000
35,644,000
35,645,000
BigWig
10
RPM
0
Pou5f1
BED
BAM
Reads
50
0

Fig. S1

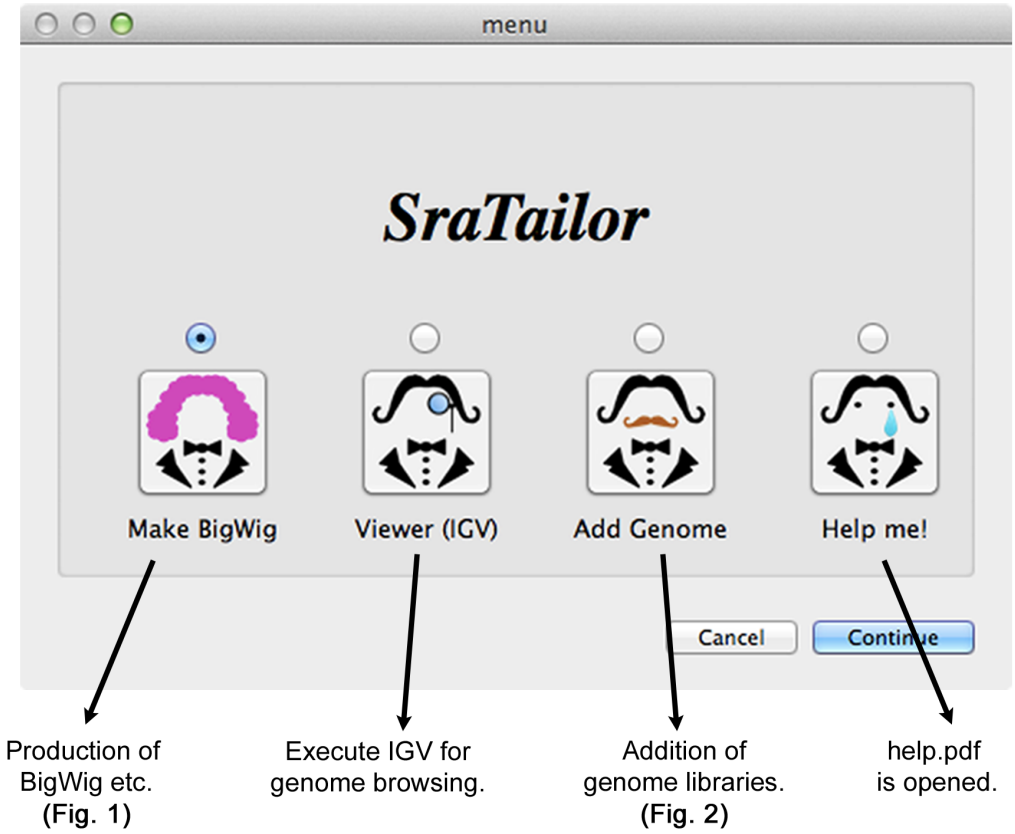
menu
SraTailor
Make BigWig
Viewer (IGV)
Add Genome
Help me!
Cancel
Continue
Production of BigWig etc. (Fig. 1)
Execute IGV for genome browsing.
Addition of genome libraries. (Fig. 2)
help.pdf is opened.

Fig. S2

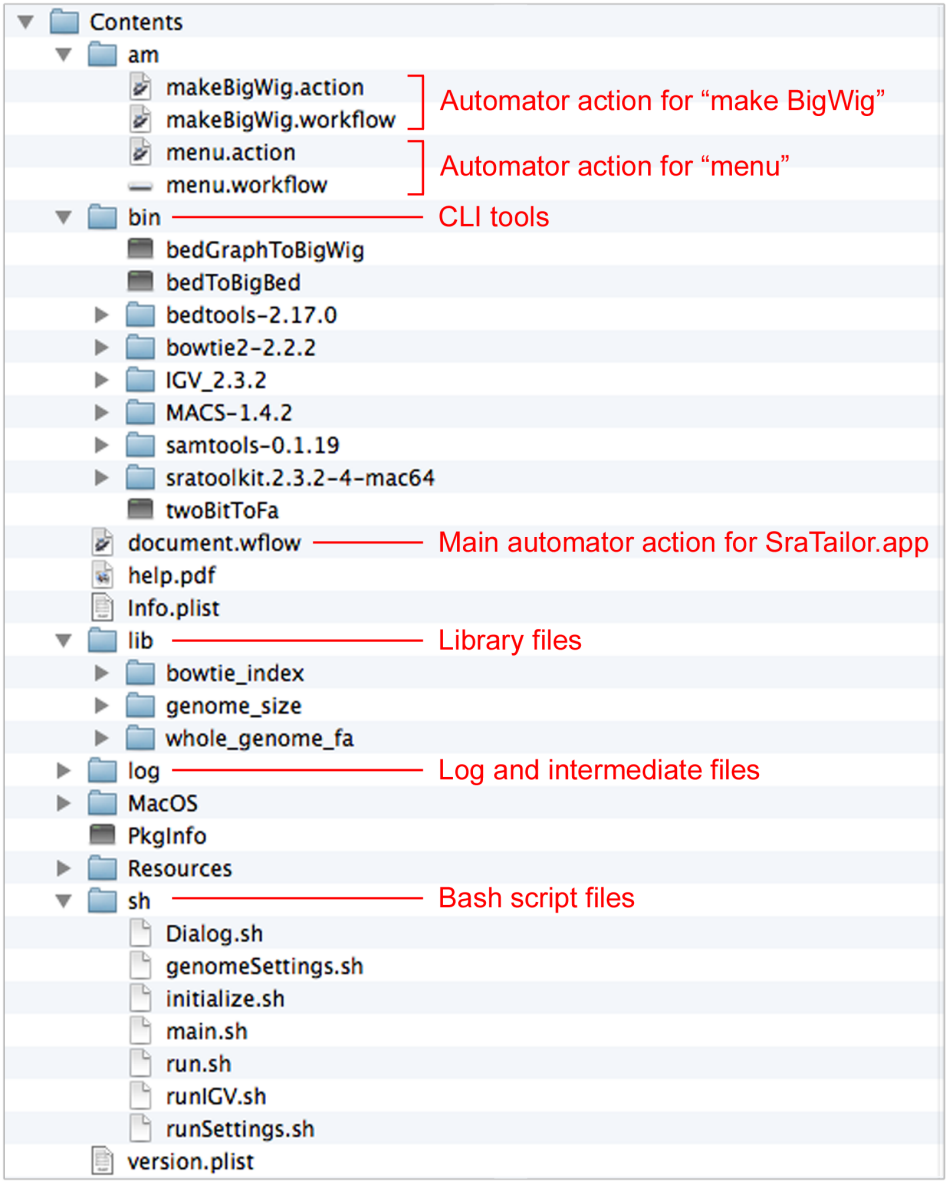
Contents
am
makeBigWig.action
makeBigWig.workflow
Automator action for “make BigWig”
menu.action
menu.workflow
Automator action for “menu”
bin
CLI tools
bedGraphToBigWig
bedToBigBed
bedtools-2.17.0
bowtie2-2.2.2
IGV_2.3.2
MACS-1.4.2
samtools-0.1.19
sratoolkit.2.3.2-4-mac64
twoBitToFa
document.wflow
Main automator action for SraTailor.app
help.pdf
Info.plist
lib
Library files
bowtie_index
genome_size
whole_genome_fa
log
Log and intermediate files
MacOS
PkgInfo
Resources
sh
Bash script files
Dialog.sh
genomeSettings.sh
initialize.sh
main.sh
run.sh
runIGV.sh
runSettings.sh
version.plist

Fig. S3

Document S1

System requirements

A Mac with a 64-bit processor is required. Windows and Linux are unsupported. Recommended and tested systems are as follows.

	Recommended	Tested
OS	Mac OS 10.8 or later	10.9.1, 10.8.4, 10.7.5, 10.6.8[a]
CPU	Intel Core i5 or later	Intel Core i5, Core 2 Duo
RAM	4GB or more	8, 4, 2[b] GB

a, Maybe imcompatible; b, too slow.

Prior to establishing the initial settings of SraTailor, Xcode (Command line tools) and Aspera Connect must be installed; both are freely available. Installation of these software packages is described in the SraTailor instruction manual, which is available on our web site (http://www.dev.med.kyushu-u.ac.jp/manual/).

Supported dataset types

SraTailor can process standard sequence data that are directly mapped onto a specified genome assembly. Therefore, SraTailor does not accept SRAs derived from reads containing technical sequences (e.g. barcode and index tags) or intra-genomic ligations (e.g., chromosome conformation capture experiments). However, technical sequences may be removed by setting Bowtie options (`-5` or `-3`). SraTailor automatically discerns single or paired reads for a specified GSM number by accessing the corresponding metadata web page. Paired reads are mapped by bowtie2 in paired-end mode (`-1` and `-2` inputs) to produce the SAM and BAM files; however, in the resultant BigWig, BedGraph, and peak files, the inserts of the paired ends are excluded. Colorspace sequences used in the SOLiD platform are unsupported.